



(A) Jobling, Stephen Alan
(B) Safford, Richard

Improvements in or Relating to Starch Content of Plants

- <130> Case 1637
- <140> US 09/297,703
- <141> 1999-07-19
- <150> PCT/GB97/03032
- <151> 1997-11-04
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- <312> 1998-05-14
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Phe Pro Cys Ala Pro Leu Cys Lys Ser Gln Ser Thr Gly Phe His Gly
15 20 25

tat cgg agg acc tcc tct tgc ctt tcc ttc aac ttc aag gag gcg ttt 146
Tyr Arg Arg Thr Ser Ser Cys Leu Ser Phe Asn Phe Lys Glu Ala Phe
30 35 40

tct agg agg gtc ttc tct gga aag tca tct cat gaa tct gac tcc tca 194
Ser Arg Arg Val Phe Ser Gly Lys Ser Ser His Glu Ser Asp Ser Ser
45 50 55

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Asn Val Met Val Thr Ala Ser Lys Arg Val Leu Pro Asp Gly Arg Ile

60	65	70	
gaa tgc tat tct tct tca aca gat caa ttg gaa gcc cct ggc aca gtt Glu Cys Tyr Ser Ser Ser Thr Asp Gln Leu Glu Ala Pro Gly Thr Val 75 80 85 90			290
tca gaa gaa tcc cag gtg ctt act gat gtt gag agt ctc att atg gat Ser Glu Glu Ser Gln Val Leu Thr Asp Val Glu Ser Leu Ile Met Asp 95 100 105			338
gat aag att gtt gaa gat gaa gta aat aaa gaa tct gtt cca atg cgg Asp Lys Ile Val Glu Asp Glu Val Asn Lys Glu Ser Val Pro Met Arg 110 115 120			386
gag aca gtt agc atc aga aaa att gga tct aaa cca agg tcc att cct Glu Thr Val Ser Ile Arg Lys Ile Gly Ser Lys Pro Arg Ser Ile Pro 125 130 135			434
cca ccc ggc aga ggg caa aga ata tat gac ata gat cca agc ttg aca Pro Pro Gly Arg Gly Gln Arg Ile Tyr Asp Ile Asp Pro Ser Leu Thr 140 145 150			482
ggc ttt cgt caa cac cta gat tac cgg tat tca cag tac aaa aga ctc Gly Phe Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr Lys Arg Leu 155 160 165 170			530
cga gaa gaa att gac aag tat gaa ggt agt ctg gat gca ttt tct cgt Arg Glu Glu Ile Asp Lys Tyr Glu Gly Ser Leu Asp Ala Phe Ser Arg 175 180 185			578
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aat aac tgg aat cct aat gca gat gtc atg act cag aat gag tgt ggt Asn Asn Trp Asn Pro Asn Ala Asp Val Met Thr Gln Asn Glu Cys Gly 220 225 230			722
gtc tgg gag atc ttt ttg ccg aat aat gca gat ggt tca cca cca att Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Ser Pro Pro Ile 235 240 245 250			770
ccc cat ggt tct cga gta aag ata cgc atg gat act cca tct ggc aac Pro His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser Gly Asn 255 260 265			818
aaa gat tct att cct gct tgg atc aag ttc tca gtt caa gca cca ggt Lys Asp Ser Ile Pro Ala Trp Ile Lys Phe Ser Val Gln Ala Pro Gly 270 275 280			866
gaa ctc cca tat aat ggc ata tac tat gat cct ccc gag gag gag aag Glu Leu Pro Tyr Asn Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Glu Lys 285 290 295			914

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Tyr Val Phe Lys Asn Pro Gln Pro Lys Arg Pro Lys Ser Leu Arg Ile	
300 305 310	
tat gag tcg cac gtt gga atg agt agt acg gag cca gta att aac aca	1010
Tyr Glu Ser His Val Gly Met Ser Ser Thr Glu Pro Val Ile Asn Thr	
315 320 325 330	
tat gcc aac ttt aga gat gat gtg ctt cct cgc atc aaa aag ctt ggc	1058
Tyr Ala Asn Phe Arg Asp Asp Val Leu Pro Arg Ile Lys Lys Leu Gly	
335 340 345	
tac aat gct gtt cag ctc atg gct att caa gag cat tca tat tat gct	1106
Tyr Asn Ala Val Gln Leu Met Ala Ile Gln Glu His Ser Tyr Tyr Ala	
350 355 360	
agt ttt ggg tat cac gtc aca aac ttt tat gca gct agc agc cga ttt	1154
Ser Phe Gly Tyr His Val Thr Asn Phe Tyr Ala Ala Ser Ser Arg Phe	
365 370 375	
gga act cct gat gat tta aag tct cta ata gat aaa gct cac gag tta	1202
Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu	
380 385 390	
ggg ctt ctt gtt ctc atg gat att gtt cat agc cat gca tca act aat	1250
Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser Thr Asn	
395 400 405 410	
acg ttg gat ggg ctg aat atg ttt gat ggt acg gat ggt cac tac ttt	1298
Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Gly His Tyr Phe	
415 420 425	
cac tct gga cca cgg ggt cat cat tgg atg tgg gac tct cgc ctt ttc	1346
His Ser Gly Pro Arg Gly His His Trp Met Trp Asp Ser Arg Leu Phe	
430 435 440	
aac tat ggg agc tgg gag gtt cta agg ttt ctt ctt tca aat gca agg	1394
Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg	
445 450 455	
tgg tgg ttg gat gag tac aag ttt gat ggg ttc aga ttt gat ggg gtg	1442
Trp Trp Leu Asp Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly Val	
460 465 470	
act tca atg atg tac acc cat cat gga ttg cag gta gat ttt acc ggc	1490
Thr Ser Met Met Tyr Thr His His Gly Leu Gln Val Asp Phe Thr Gly	
475 480 485 490	
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Asn Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Val	
495 500 505	
tat ttg atg ctg ttg aat gat atg att cat ggt ctc ttc cca gag gct	1586
Tyr Leu Met Leu Leu Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala	
510 515 520	

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gtt gaa gat ggt ggt gtt ggc ttt gat tat cgt ctc cac atg gct gtt Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Val 540 545 550	1682
gct gat aaa tgg gtt gag att att cag aag aga gat gaa gat tgg aaa Ala Asp Lys Trp Val Glu Ile Ile Gln Lys Arg Asp Glu Asp Trp Lys 555 560 565 570	1730
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cat ctg aga tat cat gga atg caa gag ttt gat caa gca att cag cat His Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Ile Gln His 700 705 710	2162
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cgg aag gat gaa agg gat cgg atc att gtc ttc gag agg gga aac ctc Arg Lys Asp Glu Arg Asp Arg Ile Ile Val Phe Glu Arg Gly Asn Leu 735 740 745	2258
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Val Phe Val Phe Asn Phe His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg
 750 755 760

gtt ggc tgc tta aag cca gga aag tac aag ata gtc ttg gat tca gat 2354
 Val Gly Cys Leu Lys Pro Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp
 765 770 775

gat cct ttg ttt gga ggc ttt ggc agg ctt agt cat gat gca gag cac 2402
 Asp Pro Leu Phe Gly Gly Phe Gly Arg Leu Ser His Asp Ala Glu His
 780 785 790

ttc agc ttt gaa ggg tgg tac gat aac cgg cct cga tcc ttc atg gtg 2450
 Phe Ser Phe Glu Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val
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 Tyr Thr Pro Cys Arg Thr Ala Val Val Tyr Ala Leu Val Glu Asp Glu
 815 820 825

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 Val Glu Asn Glu Leu Glu Pro Val Ala Gly
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Gly	Lys	Ser	Ser	His	Glu	Ser	Asp	Ser	Ser	Asn	Val	Met	Val	Thr	Ala	50	55	60	
Ser	Lys	Arg	Val	Leu	Pro	Asp	Gly	Arg	Ile	Glu	Cys	Tyr	Ser	Ser	Ser	65	70	75	80
Thr	Asp	Gln	Leu	Glu	Ala	Pro	Gly	Thr	Val	Ser	Glu	Glu	Ser	Gln	Val	85	90	95	
Leu	Thr	Asp	Val	Glu	Ser	Leu	Ile	Met	Asp	Asp	Lys	Ile	Val	Glu	Asp	100	105	110	
Glu	Val	Asn	Lys	Glu	Ser	Val	Pro	Met	Arg	Glu	Thr	Val	Ser	Ile	Arg	115	120	125	
Lys	Ile	Gly	Ser	Lys	Pro	Arg	Ser	Ile	Pro	Pro	Pro	Gly	Arg	Gly	Gln	130	135	140	
Arg	Ile	Tyr	Asp	Ile	Asp	Pro	Ser	Leu	Thr	Gly	Phe	Arg	Gln	His	Leu	145	150	155	160
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Tyr	Glu	Gly	Ser	Leu	Asp	Ala	Phe	Ser	Arg	Gly	Tyr	Glu	Lys	Phe	Gly	180	185	190	
Phe	Ser	Arg	Ser	Glu	Thr	Gly	Ile	Thr	Tyr	Arg	Glu	Trp	Ala	Pro	Gly	195	200	205	
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Pro	Asn	Asn	Ala	Asp	Gly	Ser	Pro	Pro	Ile	Pro	His	Gly	Ser	Arg	Val	245	250	255	
Lys	Ile	Arg	Met	Asp	Thr	Pro	Ser	Gly	Asn	Lys	Asp	Ser	Ile	Pro	Ala	260	265	270	
Trp	Ile	Lys	Phe	Ser	Val	Gln	Ala	Pro	Gly	Glu	Leu	Pro	Tyr	Asn	Gly	275	280	285	
Ile	Tyr	Tyr	Asp	Pro	Pro	Glu	Glu	Glu	Lys	Tyr	Val	Phe	Lys	Asn	Pro	290	295	300	
Gln	Pro	Lys	Arg	Pro	Lys	Ser	Leu	Arg	Ile	Tyr	Glu	Ser	His	Val	Gly	305	310	315	320
Met	Ser	Ser	Thr	Glu	Pro	Val	Ile	Asn	Thr	Tyr	Ala	Asn	Phe	Arg	Asp	325	330	335	

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Met Ala Ile Gln Glu His Ser Tyr Tyr Ala Ser Phe Gly Tyr His Val	355	360	365
Thr Asn Phe Tyr Ala Ala Ser Ser Arg Phe Gly Thr Pro Asp Asp Leu	370	375	380
Lys Ser Leu Ile Asp Lys Ala His Glu Leu Gly Leu Leu Val Leu Met	385	390	395
Asp Ile Val His Ser His Ala Ser Thr Asn Thr Leu Asp Gly Leu Asn	405	410	415
Met Phe Asp Gly Thr Asp Gly His Tyr Phe His Ser Gly Pro Arg Gly	420	425	430
His His Trp Met Trp Asp Ser Arg Leu Phe Asn Tyr Gly Ser Trp Glu	435	440	445
Val Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp Trp Leu Asp Glu Tyr	450	455	460
Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Met Tyr Thr	465	470	475
His His Gly Leu Gln Val Asp Phe Thr Gly Asn Tyr Asn Glu Tyr Phe	485	490	495
Gly Tyr Ala Thr Asp Val Asp Ala Val Val Tyr Leu Met Leu Leu Asn	500	505	510
Asp Met Ile His Gly Leu Phe Pro Glu Ala Val Thr Ile Gly Glu Asp	515	520	525
Val Ser Gly Met Pro Thr Val Cys Ile Pro Val Glu Asp Gly Gly Val	530	535	540
Gly Phe Asp Tyr Arg Leu His Met Ala Val Ala Asp Lys Trp Val Glu	545	550	555
Ile Ile Gln Lys Arg Asp Glu Asp Trp Lys Met Gly Asp Ile Val His	565	570	575
Met Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys Val Ser Tyr Ala Glu	580	585	590
Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala Phe Trp Leu	595	600	605
Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr	610	615	620
Pro Leu Ile Asp Arg Gly Val Ala Leu His Lys Met Ile Arg Leu Ile	625	630	635
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Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu
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 Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Asp Leu His Leu
 660 665 670
 Pro Ser Gly Lys Phe Val Pro Gly Asn Asn Tyr Ser Tyr Asp Lys Cys
 675 680 685
 Arg Arg Arg Phe Asp Leu Gly Asn Ser Lys His Leu Arg Tyr His Gly
 690 695 700
 Met Gln Glu Phe Asp Gln Ala Ile Gln His Leu Glu Glu Ala Tyr Gly
 705 710 715 720
 Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg Lys Asp Glu Arg Asp
 725 730 735
 Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val Phe Val Phe Asn Phe
 740 745 750
 His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg Val Gly Cys Leu Lys Pro
 755 760 765
 Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly
 770 775 780
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tctcaccgaa atg gta tac tac act gta tca ggc ata cgt ttt cct tgt	169
Met Val Tyr Tyr Thr Val Ser Gly Ile Arg Phe Pro Cys	
840 845 850	
gca cct tca ctc tac aaa tct cag ctc acc agc ttc cat ggc ggt cga	217
Ala Pro Ser Leu Tyr Lys Ser Gln Leu Thr Ser Phe His Gly Gly Arg	
855 860 865	
agg acc tct tct ggc ctt tcc ttc ctc ttg aag aag gag ctg ttt cct	265
Arg Thr Ser Ser Gly Leu Ser Phe Leu Leu Lys Lys Glu Leu Phe Pro	
870 875 880	
cgg aag atc ttt got gga aag tcc tct tat gaa tct gac tcc tca aat	313
Arg Lys Ile Phe Ala Gly Lys Ser Ser Tyr Glu Ser Asp Ser Ser Asn	
885 890 895	
tta act gtc tct gca tct gag aag gtc ctt gtt cct gat gat cag att	361
Leu Thr Val Ser Ala Ser Glu Lys Val Leu Val Pro Asp Asp Gln Ile	
900 905 910	
gat ggc tot tct tct tca aca tat caa tta gaa acc act ggc aca gtt	409
Asp Gly Ser Ser Ser Ser Thr Tyr Gln Leu Glu Thr Thr Gly Thr Val	
915 920 925 930	
ttg gag gaa tcc cag gtt ctt ggt gat gca gag agt ctt gtg atg gaa	457
Leu Glu Glu Ser Gln Val Leu Gly Asp Ala Glu Ser Leu Val Met Glu	
935 940 945	
gat gat aag aat gtt gag gag gat gaa gta aaa aaa gag tcg gtt cca	505
Asp Asp Lys Asn Val Glu Glu Asp Glu Val Lys Lys Glu Ser Val Pro	
950 955 960	
ttg cat gag aca att agc att gga aaa agt gaa tct aaa cca agg tcc	553
Leu His Glu Thr Ile Ser Ile Gly Lys Ser Glu Ser Lys Pro Arg Ser	
965 970 975	
att cct cca cct ggc agt ggg cag aga ata tat gac ata gat cca agc	601
Ile Pro Pro Pro Gly Ser Gly Gln Arg Ile Tyr Asp Ile Asp Pro Ser	
980 985 990	
ttg gca ggt ttc cgt cag cat ctt gac tac cga tat tca cag tac aaa	649
Leu Ala Gly Phe Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr Lys	
995 1000 1005 1010	
agg ctg cgt gag gaa att gac aag tat gaa ggt ggt ttg gat gca ttc	697
Arg Leu Arg Glu Glu Ile Asp Lys Tyr Glu Gly Gly Leu Asp Ala Phe	
1015 1020 1025	
tct cgt gga ttt gaa aag ttt ggt ttc tta cgc agt gaa aca gga ata	745

Ser Arg Gly Phe Glu Lys Phe Gly Phe Leu Arg Ser Glu Thr Gly Ile	
1030	1035 1040
act tat agg gaa tgg gca cct gga gct acg tgg gct gca ctt att gga	793
Thr Tyr Arg Glu Trp Ala Pro Gly Ala Thr Trp Ala Ala Leu Ile Gly	
1045	1050 1055
gat ttc aac aat tgg aat cct aat gca gat gtc atg act cgg aat gag	841
Asp Phe Asn Asn Trp Asn Pro Asn Ala Asp Val Met Thr Arg Asn Glu	
1060	1065 1070
ttt ggt gtc tgg gag att ttt ttg cca aat aac gca gat ggt tca cca	889
Phe Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Ser Pro	
1075	1080 1085 1090
cca att cct cat ggt tct cga gta aag ata cgc atg gat act cca tct	937
Pro Ile Pro His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser	
1095	1100 1105
ggc atc aaa gat tca att cct gct tgg atc aag ttc tca gtt cag gca	985
Gly Ile Lys Asp Ser Ile Pro Ala Trp Ile Lys Phe Ser Val Gln Ala	
1110	1115 1120
cct ggt gaa atc cca tac aat gcc ata tac tat gat cca cca aag gag	1033
Pro Gly Glu Ile Pro Tyr Asn Ala Ile Tyr Tyr Asp Pro Pro Lys Glu	
1125	1130 1135
gag aag tat gtg ttc aaa cat cct cag cca aag aga cca aaa tca ctt	1081
Glu Lys Tyr Val Phe Lys His Pro Gln Pro Lys Arg Pro Lys Ser Leu	
1140	1145 1150
agg att tat gaa tct cat gtt ggg atg agt agt atg gag cca ata att	1129
Arg Ile Tyr Glu Ser His Val Gly Met Ser Ser Met Glu Pro Ile Ile	
1155	1160 1165 1170
aac aca tat gcc aac ttt aga gat gat atg ctt cct cgc atc aaa aag	1177
Asn Thr Tyr Ala Asn Phe Arg Asp Asp Met Leu Pro Arg Ile Lys Lys	
1175	1180 1185
ctt ggc tac aat gct gtt cag atc atg gct att caa gag cat tcc tat	1225
Leu Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr	
1190	1195 1200
tat gct agt ttt ggg tac cat gtc aca aac ttt ttt gca cct agc agc	1273
Tyr Ala Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser	
1205	1210 1215
cga ttt gga act cct gat gat ttg aag tct tta ata gat aaa gct cat	1321
Arg Phe Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His	
1220	1225 1230
gag tta ggg ctg ctt gtt ctc atg gat att gtt cat agc cat gcg tca	1369
Glu Leu Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser	
1235	1240 1245 1250
aat aat acg ttg gat ggg ctg aac atg ttt gat ggt acg gat agt cac	1417
Asn Asn Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His	

1255	1260	1265	
tac ttc cac tcc gga tca cgg ggt cat cat tgg ttg tgg gac tct cgc Tyr Phe His Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg 1270 1275 1280			1465
ctt ttc aac tat gga agc tgg gag gtg cta aga ttt ctt ctt tca aat Leu Phe Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn 1285 1290 1295			1513
gca aga tgg tgg ttg gaa gag tac agg ttt gat ggt ttt aga ttt gat Ala Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp 1300 1305 1310			1561
ggg gtg act tcc atg atg tac act ccc cat ggg ttg cag gta gct ttt Gly Val Thr Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe 1315 1320 1325 1330			1609
act ggc aac tac aat gag tac ttt gga tat gca act gat gta gat gct Thr Gly Asn Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala 1335 1340 1345			1657
gtg att tat ttg atg ctt gtg aat gat atg att cac ggt ctt ttc cct Val Ile Tyr Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro 1350 1355 1360			1705
gag gct gtt acc att ggt gaa gat gtt agc gga aag cca aca ttt tgc Glu Ala Val Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys 1365 1370 1375			1753
att cca gtg gaa gat ggt ggt gtt gga ttt gat tac cgt ctc cac atg Ile Pro Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met 1380 1385 1390			1801
gcc att gcc gat aaa tgg att gag att ctt aag aag aga gat gag gac Ala Ile Ala Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp 1395 1400 1405 1410			1849
tgg aaa atg ggt gac att gtg cat aca ctc acc aac aga agg tgg ttg Trp Lys Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu 1415 1420 1425			1897
gaa aaa tgt gtt gct tat gct gaa agt cat gac caa gct ctt gtt ggt Glu Lys Cys Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly 1430 1435 1440			1945
gac aaa act att gca ttt tgg ctg atg gac aag gac atg tac gac ttc Asp Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe 1445 1450 1455			1993
atg gct cgt gac aga cca tct act cct ctt ata gat cgt gga ata gca Met Ala Arg Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala 1460 1465 1470			2041
ttg cac aaa atg atc agg ctt att acc atg ggc tta ggc gga gaa gga Leu His Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly 1475 1480 1485 1490			2089

tat ttg aat ttt atg gga aat gaa ttt gga cat cct gag tgg att gat Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp 1495 1500 1505	2137
ttt cca aga ggg gat cga cat ctg ccc aat ggt aaa gta att cca ggg Phe Pro Arg Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly 1510 1515 1520	2185
aac aac cac agt tat gat aaa tgc cgt cgt aga ttt gat cta ggt gat Asn Asn His Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp 1525 1530 1535	2233
gca gac tat cta aga tat cat gga atg caa gag ttt gat cag gca atg Ala Asp Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met 1540 1545 1550	2281
caa cat ctt gaa gaa gcc tat ggt ttc atg act tct gag cac cag tat Gln His Leu Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr 1555 1560 1565 1570	2329
ata tca cgg aag gat gaa gga gat cgg atc att gtc ttt gag agg gga Ile Ser Arg Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly 1575 1580 1585	2377
aac ctt gtt ttt gta ttc aac ttt cat tgg act aac agc tat tca gat Asn Leu Val Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp 1590 1595 1600	2425
tac cga gtt ggc tgc ttc aag tca gga aag tac aag att gtt ttg gac Tyr Arg Val Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp 1605 1610 1615	2473
tcg gat gat ggc ttg ttt gga ggc ttc aac agg ctt agt cat gat gcc Ser Asp Asp Gly Leu Phe Gly Gly Phe Asn Arg Leu Ser His Asp Ala 1620 1625 1630	2521
gag cac ttc acc ttt gac ggg tgg tat gat aac cgg cct cgg tcc ttc Glu His Phe Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe 1635 1640 1645 1650	2569
atg gta tat gca cca tct agg aca gca gtg gtc tat gct tta gta gaa Met Val Tyr Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Val Glu 1655 1660 1665	2617
gat gaa gag aat gaa gca gag aat gaa gta gaa agt gaa gtg aaa cca Asp Glu Glu Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro 1670 1675 1680	2665
gcc tcc ggc tga gatagatat tagtaagagg atccccctaaa gcaggaatgg Ala Ser Gly 1685	2717
ttaacctgtg catctgcatt gaacgacgta tattgagact tgaattgatt tgctgctcag	2777
gacacagaat attaattcca aggctcaagg cagagataca cgccataatg catgatcata	2837

tgaaagctcc ccaacttgta aatcatttag caagctgcgt gcactctgta aattatatgt	2897
agtacttttg caagtcacgt tattatggat accatggatg tccgctagga aaaattttgt	2957
gtatacgctt actaggattt ttaaactctg catgttccac ataaagtggg ggttgaatgt	3017
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<211> 848

<212> PRT

<213> Manihot, esculenta

<300>

<310> WO 98/20145

<312> 1998-05-14

<400> 31

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			20					25						30		
Ser	Gly	Leu	Ser	Phe	Leu	Leu	Lys	Lys	Glu	Leu	Phe	Pro	Arg	Lys	Ile	
		35					40						45			
Phe	Ala	Gly	Lys	Ser	Ser	Tyr	Glu	Ser	Asp	Ser	Ser	Asn	Leu	Thr	Val	
	50					55						60				
Ser	Ala	Ser	Glu	Lys	Val	Leu	Val	Pro	Asp	Asp	Gln	Ile	Asp	Gly	Ser	
	65				70					75					80	
Ser	Ser	Ser	Thr	Tyr	Gln	Leu	Glu	Thr	Thr	Gly	Thr	Val	Leu	Glu	Glu	
			85						90					95		
Ser	Gln	Val	Leu	Gly	Asp	Ala	Glu	Ser	Leu	Val	Met	Glu	Asp	Asp	Lys	
		100						105					110			
Asn	Val	Glu	Glu	Asp	Glu	Val	Lys	Lys	Glu	Ser	Val	Pro	Leu	His	Glu	
	115						120					125				
Thr	Ile	Ser	Ile	Gly	Lys	Ser	Glu	Ser	Lys	Pro	Arg	Ser	Ile	Pro	Pro	
	130					135					140					
Pro	Gly	Ser	Gly	Gln	Arg	Ile	Tyr	Asp	Ile	Asp	Pro	Ser	Leu	Ala	Gly	
	145				150				155					160		
Phe	Arg	Gln	His	Leu	Asp	Tyr	Arg	Tyr	Ser	Gln	Tyr	Lys	Arg	Leu	Arg	
			165						170					175		

Glu	Glu	Ile	Asp	Lys	Tyr	Glu	Gly	Gly	Leu	Asp	Ala	Phe	Ser	Arg	Gly	180	185	190	
Phe	Glu	Lys	Phe	Gly	Phe	Leu	Arg	Ser	Glu	Thr	Gly	Ile	Thr	Tyr	Arg	195	200	205	
Glu	Trp	Ala	Pro	Gly	Ala	Thr	Trp	Ala	Ala	Leu	Ile	Gly	Asp	Phe	Asn	210	215	220	
Asn	Trp	Asn	Pro	Asn	Ala	Asp	Val	Met	Thr	Arg	Asn	Glu	Phe	Gly	Val	225	230	235	240
Trp	Glu	Ile	Phe	Leu	Pro	Asn	Asn	Ala	Asp	Gly	Ser	Pro	Pro	Ile	Pro	245	250	255	
His	Gly	Ser	Arg	Val	Lys	Ile	Arg	Met	Asp	Thr	Pro	Ser	Gly	Ile	Lys	260	265	270	
Asp	Ser	Ile	Pro	Ala	Trp	Ile	Lys	Phe	Ser	Val	Gln	Ala	Pro	Gly	Glu	275	280	285	
Ile	Pro	Tyr	Asn	Ala	Ile	Tyr	Tyr	Asp	Pro	Pro	Lys	Glu	Glu	Lys	Tyr	290	295	300	
Val	Phe	Lys	His	Pro	Gln	Pro	Lys	Arg	Pro	Lys	Ser	Leu	Arg	Ile	Tyr	305	310	315	320
Glu	Ser	His	Val	Gly	Met	Ser	Ser	Met	Glu	Pro	Ile	Ile	Asn	Thr	Tyr	325	330	335	
Ala	Asn	Phe	Arg	Asp	Asp	Met	Leu	Pro	Arg	Ile	Lys	Lys	Leu	Gly	Tyr	340	345	350	
Asn	Ala	Val	Gln	Ile	Met	Ala	Ile	Gln	Glu	His	Ser	Tyr	Tyr	Ala	Ser	355	360	365	
Phe	Gly	Tyr	His	Val	Thr	Asn	Phe	Phe	Ala	Pro	Ser	Ser	Arg	Phe	Gly	370	375	380	
Thr	Pro	Asp	Asp	Leu	Lys	Ser	Leu	Ile	Asp	Lys	Ala	His	Glu	Leu	Gly	385	390	395	400
Leu	Leu	Val	Leu	Met	Asp	Ile	Val	His	Ser	His	Ala	Ser	Asn	Asn	Thr	405	410	415	
Leu	Asp	Gly	Leu	Asn	Met	Phe	Asp	Gly	Thr	Asp	Ser	His	Tyr	Phe	His	420	425	430	
Ser	Gly	Ser	Arg	Gly	His	His	Trp	Leu	Trp	Asp	Ser	Arg	Leu	Phe	Asn	435	440	445	
Tyr	Gly	Ser	Trp	Glu	Val	Leu	Arg	Phe	Leu	Leu	Ser	Asn	Ala	Arg	Trp	450	455	460	
Trp	Leu	Glu	Glu	Tyr	Arg	Phe	Asp	Gly	Phe	Arg	Phe	Asp	Gly	Val	Thr	465	470	475	480

Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe Thr Gly Asn
 485 490 495
 Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Ile Tyr
 500 505 510
 Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala Val
 515 520 525
 Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys Ile Pro Val
 530 535 540
 Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile Ala
 545 550 555 560
 Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp Trp Lys Met
 565 570 575
 Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys
 580 585 590
 Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr
 595 600 605
 Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala Arg
 610 615 620
 Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His Lys
 625 630 635 640
 Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn
 645 650 655
 Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg
 660 665 670
 Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly Asn Asn His
 675 680 685
 Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr
 690 695 700
 Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His Leu
 705 710 715 720
 Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg
 725 730 735
 Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val
 740 745 750
 Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Arg Val
 755 760 765
 Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp
 770 775 780

Gly Leu Phe Gly Gly Phe Asn Arg Leu Ser His Asp Ala Glu His Phe
785 790 795 800

Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr
805 810 815

Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Val Glu Asp Glu Glu
820 825 830

Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro Ala Ser Gly
835 840 845

<210> 32

<211> 48

<212> DNA

<213> Manihot, esculenta

<300>

<310> WO 98/20145

<312> 1998-05-14

<400> 32

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48

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<212> DNA

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<221> CDS

<222> 1..687

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<312> 1998-05-14

<400> 33

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Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr
1 5 10 15

48

cct ctc ata gat cgt gga gta gca ttg cac aaa atg atc agg ctt att

96

Pro Leu Ile Asp Arg Gly Val Ala Leu His Lys Met Ile Arg Leu Ile	
20 25 30	
acc atg gga tta ggc gga gaa gga tat ttg aat ttt atg gga aat gaa	144
Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu	
35 40 45	
ttt gga cac ccc gag tgg att gat ttt cca aga ggt gat cta cat ctt	192
Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Asp Leu His Leu	
50 55 60	
ccc agt ggt aaa ttt gtt cct ggg aac aat tac agt tat gat aaa tgc	240
Pro Ser Gly Lys Phe Val Pro Gly Asn Asn Tyr Ser Tyr Asp Lys Cys	
65 70 75 80	
cgg cgt agg ttt gat cta ggc aat tca aag cgt ctg aga tat cat gga	288
Arg Arg Arg Phe Asp Leu Gly Asn Ser Lys Arg Leu Arg Tyr His Gly	
85 90 95	
atg caa gag ttt gat caa gca att cag cat ctt gaa gaa gcc tat ggt	336
Met Gln Glu Phe Asp Gln Ala Ile Gln His Leu Glu Glu Ala Tyr Gly	
100 105 110	
ttc atg act tct gag cac caa tac ata tca cgg aag gat gaa agg gat	384
Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg Lys Asp Glu Arg Asp	
115 120 125	
cgg atc att gtc ttc gag agg gga aac ctc gtt ttt gta ttc aat ttt	432
Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val Phe Val Phe Asn Phe	
130 135 140	
cat tgg act agc agc tat tcg gat tac cga gtt ggc tgc tta aag cca	480
His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg Val Gly Cys Leu Lys Pro	
145 150 155 160	
gga aag tac aag ata gtc ttg gat tca gat gat cct ttg ttt gga ggc	528
Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly	
165 170 175	
ttt ggc agg ctt agt cat gat gca gag cac ttc agc ttt gaa ggg tgg	576
Phe Gly Arg Leu Ser His Asp Ala Glu His Phe Ser Phe Glu Gly Trp	
180 185 190	
tac gat aac cgg cct cga tcc ttc atg gtg tac aca cca tgt aga aca	624
Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr Thr Pro Cys Arg Thr	
195 200 205	
gca gtg gtc tat gct tta gtg gag gat gaa gtg gag aat gaa gtg gaa	672
Ala Val Val Tyr Ala Leu Val Glu Asp Glu Val Glu Asn Glu Val Glu	
210 215 220	
cct gtc gcc ggt taa gatatatcctt agcaacaggt tctgaagcag gaatgccatt	727
Pro Val Ala Gly	
225	
attgatcttc ctatgtgcat ctgcgttgaa cgaaatatat tgagcctata atttgatgtc	787

acgggccttg cagatttcca tcctggttct tgggtatttg ttgtcatgat aaacataatc 847
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 ctccctaaacc ataaatcttc aagctgcctg cggtcggtag tatgttatgt ggtactttgc 967
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<211> 228

<212> PRT

<213> Manihot, esculenta

<300>

<310> WO 98/20145

<312> 1998-05-14

<400> 34

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Pro Leu Ile Asp Arg Gly Val Ala Leu His Lys Met Ile Arg Leu Ile
 20 25 30

Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu
 35 40 45

Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Asp Leu His Leu
 50 55 60

Pro Ser Gly Lys Phe Val Pro Gly Asn Asn Tyr Ser Tyr Asp Lys Cys
 65 70 75 80

Arg Arg Arg Phe Asp Leu Gly Asn Ser Lys Arg Leu Arg Tyr His Gly
 85 90 95

Met Gln Glu Phe Asp Gln Ala Ile Gln His Leu Glu Glu Ala Tyr Gly
 100 105 110

Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg Lys Asp Glu Arg Asp
 115 120 125

Arg Ile Ile Val Phe Glu Arg Gly Asn Leu Val Phe Val Phe Asn Phe
 130 135 140

His Trp Thr Ser Ser Tyr Ser Asp Tyr Arg Val Gly Cys Leu Lys Pro
 145 150 155 160

Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly
 165 170 175

Phe Gly Arg Leu Ser His Asp Ala Glu His Phe Ser Phe Glu Gly Trp
180 185 190

Tyr Asp Asn Arg Pro Arg Ser Phe Met Val Tyr Thr Pro Cys Arg Thr
195 200 205

Ala Val Val Tyr Ala Leu Val Glu Asp Glu Val Glu Asn Glu Val Glu
210 215 220

Pro Val Ala Gly
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<210> 35

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<212> DNA

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<221> CDS

<222> 61..1506

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<312> 1998-05-14

<400> 35

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Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe
230 235 240 245

gga act cct gat gat ttg aag tct tta ata gat aaa gct cat gag tta 156
Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu
250 255 260

ggg ctg ctt gtt ctc atg gat att gtt cat agc cat gcg tca aat aat 204
Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ala Ser Asn Asn
265 270 275

acg ttg gat ggg ctg aac atg ttt gat ggt acg gat agt cac tac ttc 252
Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His Tyr Phe
280 285 290

cac tcc gga tca cgg ggt cat cat tgg ttg tgg gac tct cgc ctt ttc 300
His Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg Leu Phe
295 300 305

aac tat gga agc tgg gag gtg cta aga ttt ctt ctt tca aat gca aga 348

Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg	
310 315 320 325	
tgg tgg ttg gaa gag tac agg ttt gat ggt ttt aga ttt gat ggg gtg	396
Trp Trp Leu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val	
330 335 340	
act tcc atg atg tac act ccc cat ggg ttg cag gta gct ttt act ggc	444
Thr Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe Thr Gly	
345 350 355	
aac tac aat gag tac ttt gga tat gca act gat gta gat gct gtg att	492
Asn Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Ile	
360 365 370	
tat ttg atg ctt gtg aat gat atg att cac ggt ctt ttc cct gag gct	540
Tyr Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala	
375 380 385	
gtt acc att ggt gaa gat gtt agc gga aag cca aca ttt tgc att cca	588
Val Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys Ile Pro	
390 395 400 405	
gtg gaa gat ggt ggt gtt gga ttt gat tac cgt ctc cac atg gcc att	636
Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile	
410 415 420	
gcc gat aaa tgg att gag att ctt aag aag aga gat gag gac tgg aaa	684
Ala Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp Trp Lys	
425 430 435	
atg ggt gac att gtg cat aca ctc acc aac aga agg tgg ttg gaa aaa	732
Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys	
440 445 450	
tgt gtt gct tat gct gaa agt cat gac caa gct ctt gtt ggt gac aaa	780
Cys Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys	
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act att gca ttt tgg ctg atg gac aag gac atg tac gac ttc atg gct	828
Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala	
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Arg Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His	
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Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu	
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aat ttt atg gga aat gaa ttt gga cat cct gag tgg att gat ttt cca	972
Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro	
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Arg Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly Asn Asn	

535

540

545

cac agt tat gat aaa tgc cgt cgt aga ttt gat cta ggt gat gca gac 1068
 His Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp
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 Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His
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 Leu Glu Glu Ala Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser
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 Arg Lys Asp Glu Gly Asp Arg Ile Ile Val Phe Glu Arg Gly Asn Leu
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 Phe Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val
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 Tyr Ala Pro Ser Arg Thr Ala Val Val His Ala Leu Val Glu Asp Glu
 680 685 690

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 Glu Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro Ala Ser
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 Gly
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Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser His Tyr Phe
50 55 60

His Ser Gly Ser Arg Gly His His Trp Leu Trp Asp Ser Arg Leu Phe
65 70 75 80

Asn Tyr Gly Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala Arg
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Trp Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val
100 105 110

Thr Ser Met Met Tyr Thr Pro His Gly Leu Gln Val Ala Phe Thr Gly
115 120 125

Asn Tyr Asn Glu Tyr Phe Gly Tyr Ala Thr Asp Val Asp Ala Val Ile
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Tyr Leu Met Leu Val Asn Asp Met Ile His Gly Leu Phe Pro Glu Ala
145 150 155 160

Val Thr Ile Gly Glu Asp Val Ser Gly Lys Pro Thr Phe Cys Ile Pro
165 170 175

Val Glu Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile
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Ala Asp Lys Trp Ile Glu Ile Leu Lys Lys Arg Asp Glu Asp Trp Lys
195 200 205

Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys
 210 215 220
 Cys Val Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys
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 Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala
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 Arg Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His
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 Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu
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 Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro
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 Arg Gly Asp Arg His Leu Pro Asn Gly Lys Val Ile Pro Gly Asn Asn
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 325 330 335
 Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His
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 385 390 395 400
 Val Gly Cys Phe Lys Ser Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp
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 Phe Thr Phe Asp Gly Trp Tyr Asp Asn Arg Pro Arg Ser Phe Met Val
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 Glu Asn Glu Ala Glu Asn Glu Val Glu Ser Glu Val Lys Pro Ala Ser
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 Gly